method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a host cell (eukaryotic, such as plant or yeast, prokaryotic such as bacterial, or viral) may comprise the steps of: constructing an isolated polynucleotide of the present invention or an isolated chimeric gene of the present invention; introducing the isolated polynucleotide or the isolated chimeric gene into a host cell; measuring the level a polypeptide in the host cell containing the isolated polynucleotide; and comparing the level of a polypeptide in the host cell containing the isolated polynucleotide with the level of a polypeptide in a host cell that does not contain the isolated polynucleotide.

Paragraph starting at page 9, line 17.

"Codon degeneracy" refers to divergence in the genetic code permitting variation of the nucleotide sequence without affecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention relates to any nucleic acid fragment comprising a nucleotide sequence that encodes all or a substantial portion of the amino acid sequences set forth herein. The skilled artisan is well aware of the "codon-bias" exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid fragment for improved expression in a host cell, it is desirable to design the nucleic acid fragment such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

IN THE CLAIMS:

Please cancel claims 1-23.

Please add the following new claims:

--24. An isolated polynucleotide that encodes an Mlo homolog polypeptide having a sequence identity of at least 85%, based on the Clustal method of alignment, when compared to a polypeptide selected from the group consisting of SEQ ID NOs: SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.

25. The polynucleotide of Claim 24 wherein the sequence identity is at least 90%.

26. The polynucleotide of Claim 24 wherein the sequence identity is at least 95%.

27. The polynucleotide of Claim 24 wherein the polypeptide is selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.

28. The polynucleotide of Claim 24, wherein the polynucleotide is selected from SEQ ID Nos:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37.

29. An isolated complement of the polynucleotide of Claim 24, wherein (a) the complement and the polynucleotide consist of the same number of nucleotides, and (b)

the nucleotide sequences of the complement and the polynucleotide have 100% complementarity.

30. An isolated nucleic acid molecule that encodes an Mlo homolog polypeptide and remains hybridized with the isolated polynucleotide of Claim 24 under a wash condition of 0.1X SSC, 0.1% SDS, and 65°C.

31. A cell or a virus comprising the polynucleotide of Claim 24.

32. The cell of Claim 33, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell, an insect cell, and a plant cell.

33. A transgenic plant comprising the polynucleotide of Claim 24.

34. A method for transforming a cell comprising introducing into a cell the polynucleotide of Claim 24.

35. A method for producing a transgenic plant comprising (a) transforming a plant cell with the polynucleotide of Claim 24, and (b) regenerating a plant from the transformed plant cell.

36. An isolated an Mlo homolog polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.

37. A chimeric gene comprising the polynucleotide of Claim 24 operably linked to at least one suitable regulatory sequence.

38. The chimeric gene of Claim 39, wherein the chimeric gene is an expression vector.

39. A method for altering the level of an Mlo homolog polypeptide expression in a host cell, the method comprising:

(a) Transforming a host cell with the chimeric gene of claim 39; and
(b) Growing the transformed cell in step (a) under conditions suitable for the expression of the chimeric gene. --